

Notice of Allowability

Application No.

10/689,461

Examiner

Delia M. Ramirez

Applicant(s)

HARRISON ET AL.

Art Unit

1652

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to 4/20/2006.
2. ☒ The allowed claim(s) is/are 8.
3. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
a) ☐ All b) ☐ Some* c) ☐ None of the:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

* Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.

THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

4. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.
5. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.
(a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached
1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.
(b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.
- Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).
6. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

1. ☒ Notice of References Cited (PTO-892)
2. ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3. ☒ Information Disclosure Statements (PTO-1449 or PTO/SB/08),
Paper No./Mail Date 12/2/04
4. ☐ Examiner's Comment Regarding Requirement for Deposit of Biological Material
5. ☐ Notice of Informal Patent Application (PTO-152)
6. ☐ Interview Summary (PTO-413),
Paper No./Mail Date _____
7. ☒ Examiner's Amendment/Comment
8. ☒ Examiner's Statement of Reasons for Allowance
9. ☒ Other alignment.

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DETAILED ACTION

Status of the Application

Claims 1-26 are pending.

Applicant's election of Group IV, claim 8, drawn to a polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 in a communication filed on 4/20/2006 is acknowledged.

Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

In a telephone conversation with Ms Jane Potter on 6/26/2006, an agreement was reached to amend the specification to correct minor errors in the specification, to amend claim 8, and to cancel non-elected claims 1-7 and 9-26 to place the application in condition for allowance.

Priority

1. Acknowledgment is made of a claim for domestic priority under 35 U.S.C. 119(e) to provisional application No. 60/221,242 filed on 07/27/2000.
2. Acknowledgment is made of a claim for domestic priority under 35 U.S.C. 120 or 121 to US application No. 10/211,412 filed on 07/31/2002, and 09/916,109 filed on 07/25/2001.
3. The polypeptide of SEQ ID NO: 2 appears to have been first disclosed in provisional application No. 60/221,242 (shown in Figure 2).

Information Disclosure Statement

4. The information disclosure statement (IDS) submitted on 12/2/2004 is acknowledged. The submission is in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Drawings

5. The drawings submitted on 10/20/2003 have been reviewed and are accepted by the Examiner.

Examiner's Amendment

6. An Examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it MUST be submitted no later than the payment of the issue fee.
7. Amendments to the specification are required to comply with sequence rules and to correct an obvious error in the sequence identifier used.
8. Authorization for this Examiner's amendment was given in a telephone interview with Ms Jane Potter on 6/26/2006.
9. Please enter the following amendments to the specification as follows:
- a. On page 9, line 11, please replace " SEQ ID NO: 8" with " SEQ ID NO: 11".
 - b. On page 14, line 9, please replace "(EYMPTD)" with "(EYMPTD)(SEQ ID NO: 10)".
10. Please cancel non-elected claims 1-7 and 9-26.
11. Please replace claim 8 as follows:
- 8. An isolated polypeptide consisting of the amino acid sequence of SEQ ID NO: 2.

Reasons for Allowance

12. The following is an Examiner's statement of reasons for allowance. Although the prior art discloses a human glycogen synthase kinase 3β , the Examiner has found no teaching or suggestion in the prior art directed to a polypeptide consisting of the amino acid sequence of SEQ ID NO: 2 (394 amino acids long). The closest homolog to the polypeptide of SEQ ID NO: 2 is the human glycogen synthase kinase 3β (GSK- 3β) taught by Stambolic et al. (PIR accession number S53324; EMBL/GenBank

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accession number P49841, October 1, 1996; cited in the IDS; see attached alignment). The polypeptide of Stambolic et al. (420 amino acids long) has 97.2% sequence identity to the polypeptide of SEQ ID NO: 2 (97.5% = $384 \times 100 / 394$). The polypeptide of SEQ ID NO: 2 comprises amino acids 1-384 of the polypeptide of Stambolic et al. Therefore, claim 8 directed to the polypeptide of SEQ ID NO: 2, is allowable over the prior art of record.

Art of Interest

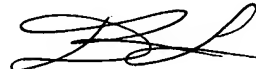
13. Bax et al. (Structure 9:1143-1152, December 2001) discloses a truncated version of human GSK-3 β which consists of amino acids 27-393 of the human GSK-3 β (420 amino acids long; PIR accession number S53324; EMBL/GenBank accession number P49841) and a histidine tag (page 1145, left column, Results, last complete paragraph).

Conclusion

14. Claim 8 is allowed.

15. Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."

16. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571) 272-1600.



Delia M. Ramirez, Ph.D.
Patent Examiner
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2006, 15:05:56 ; Search time 41 Seconds
(without alignments)
924.620 Million cell updates/sec

Title: US-10-689-461-2

Sequence: 1 MEYMPMEGSGMSGRPTTSF.....QELSSNPPLATILIPRIARI 394

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	97.3	420	1 S53324	glycogen synthase
2	2010	96.6	420	1 TVRTKB	tau-protein kinase
3	1931	92.8	420	1 S15425	intracellular kina
4	1923	92.4	420	2 S15682	glycogen synthase
5	1607	77.2	483	1 TVRTKA	protein kinase (EC
6	1590.5	76.4	575	2 S35327	protein kinase (EC
7	1542.5	74.1	733	2 S10932	probable protein k
8	1542.5	74.1	1067	2 S35423	protein kinase sgg
9	1342.5	64.5	362	2 T26520	hypothetical prote
10	1296	62.3	409	2 S51105	shaggy protein kin
11	1275.5	61.3	471	2 T03601	shaggy protein kin
12	1273.5	60.8	471	1 T02297	shaggy protein kin
13	1265	60.2	408	2 T48637	protein kinase MSK
14	1258	60.5	472	1 T01236	serine/threonine-s
15	1256	60.4	412	1 S37642	protein kinase MSK
16	1249	60.0	403	2 T03777	probable shaggy-11
17	1249	60.0	431	2 S51106	shaggy protein kin
18	1247.5	59.9	469	1 T02256	shaggy protein kin
19	1246	59.9	409	1 S41597	protein kinase ASK
20	1245	59.8	412	2 S71266	shaggy-11ke protei
21	1244	59.8	411	1 S37643	protein kinase MSK
22	1239	59.5	409	2 S52095	tau-protein kinase
23	1234	59.3	380	2 T04863	shaggy-11ke protei
24	1233	59.3	412	2 A84715	probable shaggy-11
25	1232	59.2	405	1 S41596	protein kinase ASK
26	1232	59.2	407	2 S77922	shaggy-11ke protei
27	1229.5	59.1	420	2 A96613	probable glycogen
28	1229.5	59.1	469	1 T02254	shaggy protein kin
29	1228.5	59.0	447	2 F86232	hypothetical prote

30	1226	58.9	411	1 S37644	protein kinase MSK
31	1226	58.9	469	2 T08139	shaggy-11ke protei
32	1220	58.6	421	2 S51938	protein kinase ACK
33	1208	58.0	447	2 T01756	hypothetical prote
34	1178	56.6	468	2 A55476	protein kinase (EC
35	1158	55.6	431	2 T47908	shaggy-11ke kinase
36	1156.5	55.6	387	2 T37758	protein kinase sgp
37	1109.5	53.3	354	2 T45138	protein kinase sgp
38	996	47.9	381	2 T40746	serine-threonine p
39	996	47.9	390	2 T43008	probable protein k
40	978.5	47.0	452	2 T18457	glycogen synthase
41	940.5	45.2	354	2 F90121	hypothetical prote
42	940	45.2	370	2 A56347	protein kinase RIM
43	873.5	42.0	501	2 S67615	MXK1 protein - yea
44	792	38.1	211	2 T04119	probable serine/th
45	735.5	35.3	367	2 T19937	hypothetical prote

ALIGNMENTS

RESULT 1

S53324
Glycogen synthase kinase 3 beta (EC 2.7.1.-) - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text-change 09-Jul-2004
C:Accession: S53324
R:Stambolic, V.; Woodgett, J.R.
Biochem. J. 303, 701-704, 1994
A:Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via se
A:Reference number: S53324; MIM:35071278; PMID:7960435
A:Accession: S53324
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-420 <STA>
A:Cross-references: UNIPROT: P24881; UNIPARC: UP100004E93D; EMBL: L33801; NID: G529236; PI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (se
C:Gene: GSK3B
A:Gene: GSK3B
A:Cross-references: GDB: 6108057
C:Superfamily: kinase-related, transforming protein, protein kinase homology
C:Keywords: ATP, phosphoprotein, phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status e
F:85/Active site: Lys #status predicted

Query Match	97.3%	Score 2024;	DB 1;	Length 420;
Best Local Similarity	100.0%;	Pred. No. 2, 6e-89;		
Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	11	MSGRPRTTSFAESCCKVQOQSARFSKMSKVSRTDQSGSVTTVAAPGCGPDRPOVSSTYDTK	70	
DB	1	MSGRPRTTSFAESCCKVQOQSARFSKMSKVSRTDQSGSVTTVAAPGCGPDRPOVSSTYDTK	60	
QY	71	VINGSGFGVYQAKLQDQSGELVAIKKYLQDKRPKNRELQIMRLDHCNRYRLRFFYSYG	130	
DB	61	VINGSGFGVYQAKLQDQSGELVAIKKYLQDKRKRELQIMRLDHCNRYRLRFFYSYG	120	
QY	131	EKKDQVYLVLDVDEYVETVYRVARHYSRAKQTLPVITYVKLYMTQLFSLAYIHSFGICHR	190	
DB	121	EKKDQVYLVLDVDEYVETVYRVARHYSRAKQTLPVITYVKLYMTQLFSLAYIHSFGICHR	180	
QY	191	DTRPQNLDDPPTAVAKLQDQSGAKOLVNGEPVNSYTCSSRYAAPLIPRATYTSIDV	250	
DB	181	DTRPQNLDDPPTAVAKLQDQSGAKOLVNGEPVNSYTCSSRYAAPLIPRATYTSIDV	240	
QY	251	WSAGCVLAELILGQPIFPDQSGVDQVLEIKVLGTPTREQIRRMNNPYTEFFKPKAIAP	310	
DB	241	WSAGCVLAELILGQPIFPDQSGVDQVLEIKVLGTPTREQIRRMNNPYTEFFKPKAIAP	300	
QY	311	MTKVFRRPTPEPAIALCSRLLEYTPARLUTPLAEACAHSPFDELDRPNVHGPNGRDTPALP	370	

Db 301 WTKVFRPTTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALP 360

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

RESULT 2

TVTRKB

tau-protein kinase (EC 2.7.1.135) I - rat

N:Altermate names: factor A; glycogen synthase kinase 3 beta; protein kinase GSK-3-beta;

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C/Accession: S14708; S33741; S36729

R:Woodgett, J.R.

EMBO J. 9, 2431-2438, 1990

A>Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.

A/Reference number: S14707; MUID:90316097; PMID:2164470

A/Accession: S14708

A/Molecule type: mRNA

A/Residues: 1-420 <MO>

A/Cross-references: UNIPROT:P18266; UNIPARC:UPI000012DDQ; EMBL:X53428; NID:956333; PIDN

A>Note: the author translated the codon ATG for residue 240 as Val

R:ishiguro, K.; Shitabuchi, A.; Sato, S.; Omori, A.; Arioka, M.; Kobayashi, S.; Uchida,

FEBS Lett. 325, 167-172, 1993

A>Title: Glycogen synthase kinase 3-beta is identical to tau protein kinase I generating

A/Reference number: S33741; MUID:93307488; PMID:7686508

A/Accession: S33741

A/Molecule type: protein

A/Residues: 1-239, 'V', 241-420 <ISH>

A/Cross-references: UNIPARC:UPI0000018B4; EMBL:X73653; NID:9402651; PIDN:CA52020.1; PI

A/Accession: S36729

A/Molecule type: protein

A/Residues: 37-58; 61-74; 151-158; 293-316; 318-325; 327-332; 351-368; 370-375 <ISH>

A/Cross-references: UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538;

33D

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein K

P:54-315/Domain: protein kinase homology <KIN>

P:62-70/Region: protein kinase ATP-binding motif

P:85/Active site: Lys #status predicted

Query Match 96.6%; Score 2010; DB 1; Length 420;

Best Local Similarity 99.5%; Pred. No. 1.2e-88;

Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTFAESCKPVQOPSAFGSMKVRDQSGKVTTVATPGGPDPRPQEVSYTDTK 70

Db 1 MSGRPRTTFAESCKPVQOPSAFGSMKVRDQSGKVTTVATPGGPDPRPQEVSYTDTK 60

Qy 71 VTGNSFGVYVQAKLSDSGELVAIKVLDQKRFKRELQIMKLDHCNTVRLRYFPYSSG 130

Db 61 VTGNSFGVYVQAKLSDSGELVAIKVLDQKRFKRELQIMKLDHCNTVRLRYFPYSSG 120

Qy 131 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 190

Db 121 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 180

Qy 191 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 250

Db 181 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 240

Qy 251 WSAGCVLAEILLGQPIFPDSDGVLDLVEIKVLTGPTREQIREMNPNTYEFKFPQIKAH 310

Db 241 WSAGCVLAEILLGQPIFPDSDGVLDLVEIKVLTGPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALP 370

Db 301 WTKVFRPTTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALP 360

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

RESULT 3

intracellular kinase (EC 2.7.1.-) - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: I51425

R:Pierce, S.B.; Kimmel, D.

Development 121, 755-765, 1995

A>Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.

A/Reference number: I51425; MUID:95237008; PMID:7720580

A/Accession: I51425

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-420 <PIE>

A/Cross-references: UNIPROT:Q91757; UNIPARC:UPI000005B682; GB:L38492; NID:9727189; PIDN

C/Genetics:

A:Gene: Xgsk-3

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; phosphotransferase

P:54-315/Domain: protein kinase homology <KIN>

P:62-70/Region: protein kinase ATP-binding motif

P:85/Active site: Lys #status predicted

Query Match 92.8%; Score 1911; DB 2; Length 420;

Best Local Similarity 95.3%; Pred. No. 6.5e-85;

Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 11 MSGRPRTTFAESCKPVQOPSAFGSMKVRDQSGKVTTVATPGGPDPRPQEVSYTDTK 70

Db 1 MSGRPRTTFAESCKPVQOPSAFGSMKVRDQSGKVTTVATPGGPDPRPQEVSYTDTK 60

Qy 71 VTGNSFGVYVQAKLSDSGELVAIKVLDQKRFKRELQIMKLDHCNTVRLRYFPYSSG 130

Db 61 VTGNSFGVYVQAKLSDSGELVAIKVLDQKRFKRELQIMKLDHCNTVRLRYFPYSSG 120

Qy 131 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 190

Db 121 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 180

Qy 191 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 250

Db 181 EKKDEVYLVLDYVETVYRVARHYSRAKQTLPIVYVLYQVLMYQFRLSLAYIHSFGICHR 240

Qy 251 WSAGCVLAEILLGQPIFPDSDGVLDLVEIKVLTGPTREQIREMNPNTYEFKFPQIKAH 310

Db 241 WSAGCVLAEILLGQPIFPDSDGVLDLVEIKVLTGPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALP 370

Db 301 WTKVFRPTTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALP 360

Qy 371 NFFTQELSSNPPLATLILIPPHARI 393

Db 361 NFFTQELSSNPPLATLILIPPHARI 383

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384

Qy 371 NFFTQELSSNPPLATLILIPPHARI 394

Db 361 NFFTQELSSNPPLATLILIPPHARI 384